

Name:
ID:

CSCI 3104, Algorithms
Explain-It-Back 5

Profs. Grochow & Layer
Spring 2019, CU-Boulder

At a recent infections disease seminar, you hear about how the speaker is sequencing millions of *Plasmodium falciparum* genomes (the human malaria parasite) in order to better characterize how patients respond to treatment. In the presentation, the speaker complained to the audience that although they are making the data sets as small as possible by only using 2 bits to encode the 4 nucleotides of the genomes their IT department is still struggling to store all the data. Later in the presentation, you learn that the *Plasmodium falciparum* genome is "AT-rich." That is, over 80% of the nucleotides in the genome are either A or T. Please help this team understand how they can leverage *Plasmodium falciparum*'s AT-richness to help their IT department deal with the influx of data.

Name:

ID:

CSCI 3104, Algorithms
Explain-It-Back 5

Profs. Grochow & Layer
Spring 2019, CU-Boulder
